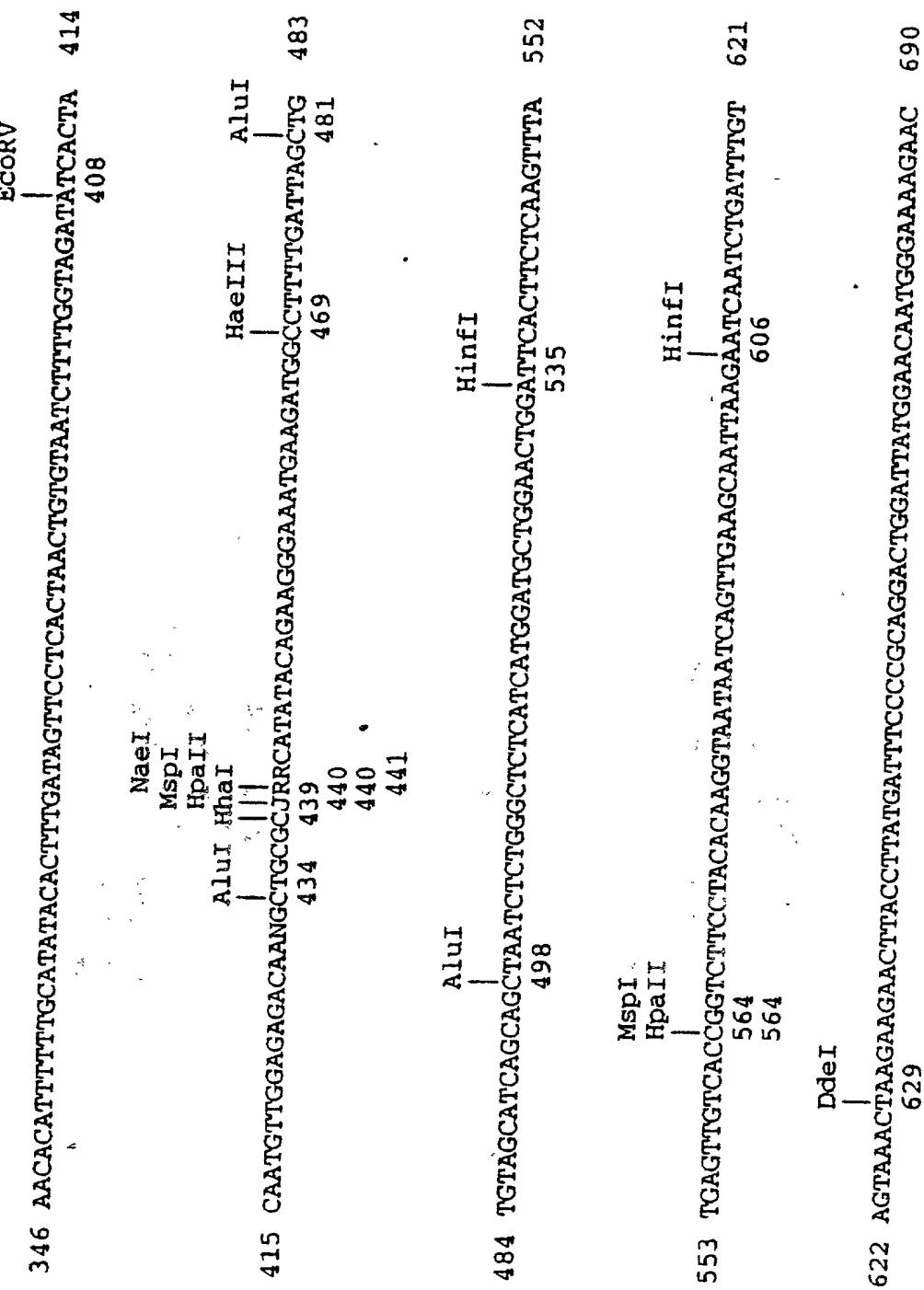


FIG. 1A

FIG. 1B



其後又作《新編卷之三》。此卷之題，即用《新編卷之三》。

760 TTAGTGAATAAACTTAATTCAAAAAGCTTCATTGACTTATATACTTGTGTGAATTGGTA 828

829 GGAACCTATTCTAGGAGTCATACAAAGTGGACTCATTTCCATTCAAGTGATAAATAAGAAA 897
 DdeI | Hinfl |
 843 | 866

XbaI	TGGAAAGAAGATTTCATGATAACCTCCATGACAACCTGGTAATCGTGGCTGGTAAATGTCGAGG	966
	909	962
TaqI		

FIG. 1C

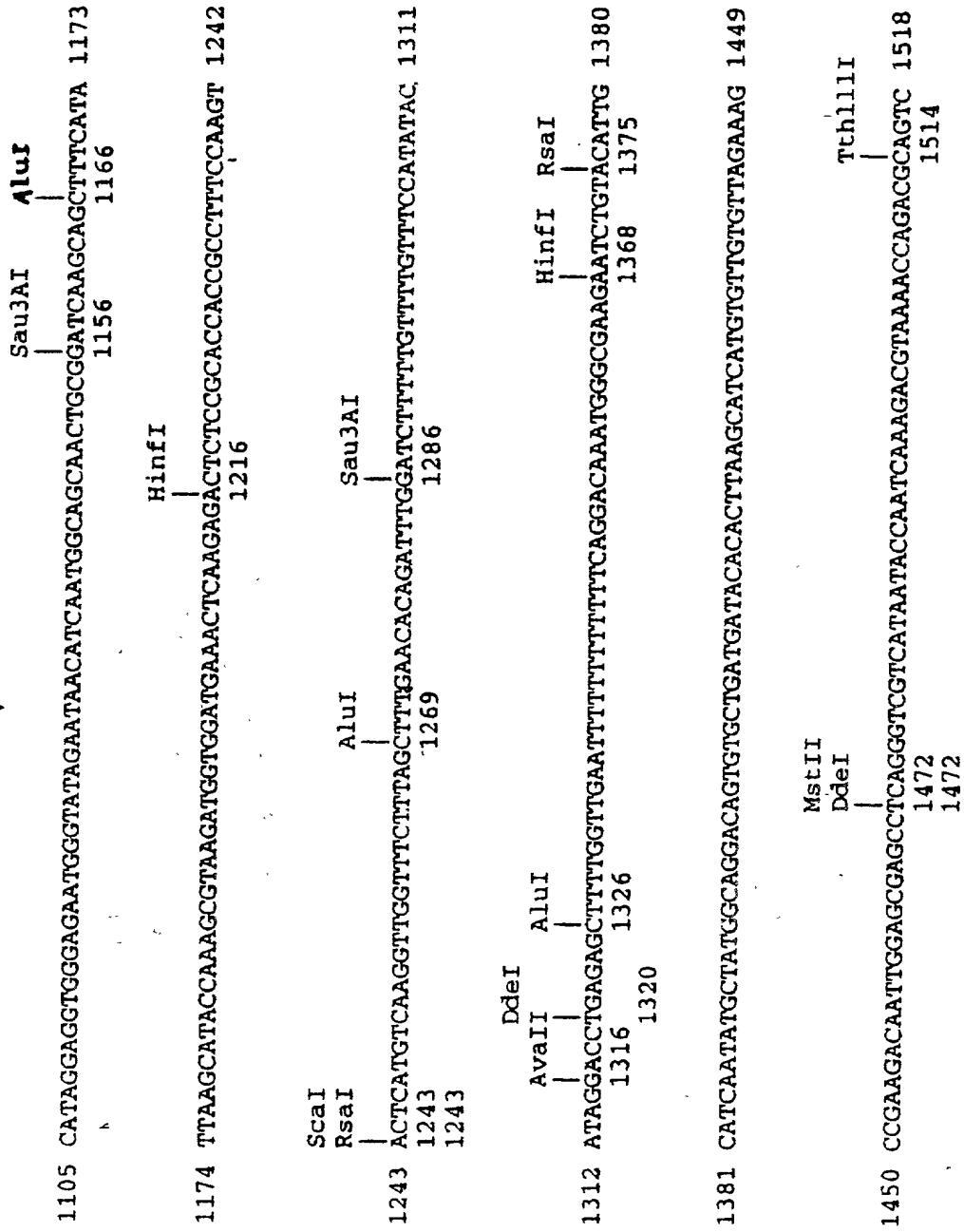


FIG. 1D

FIG. 1E

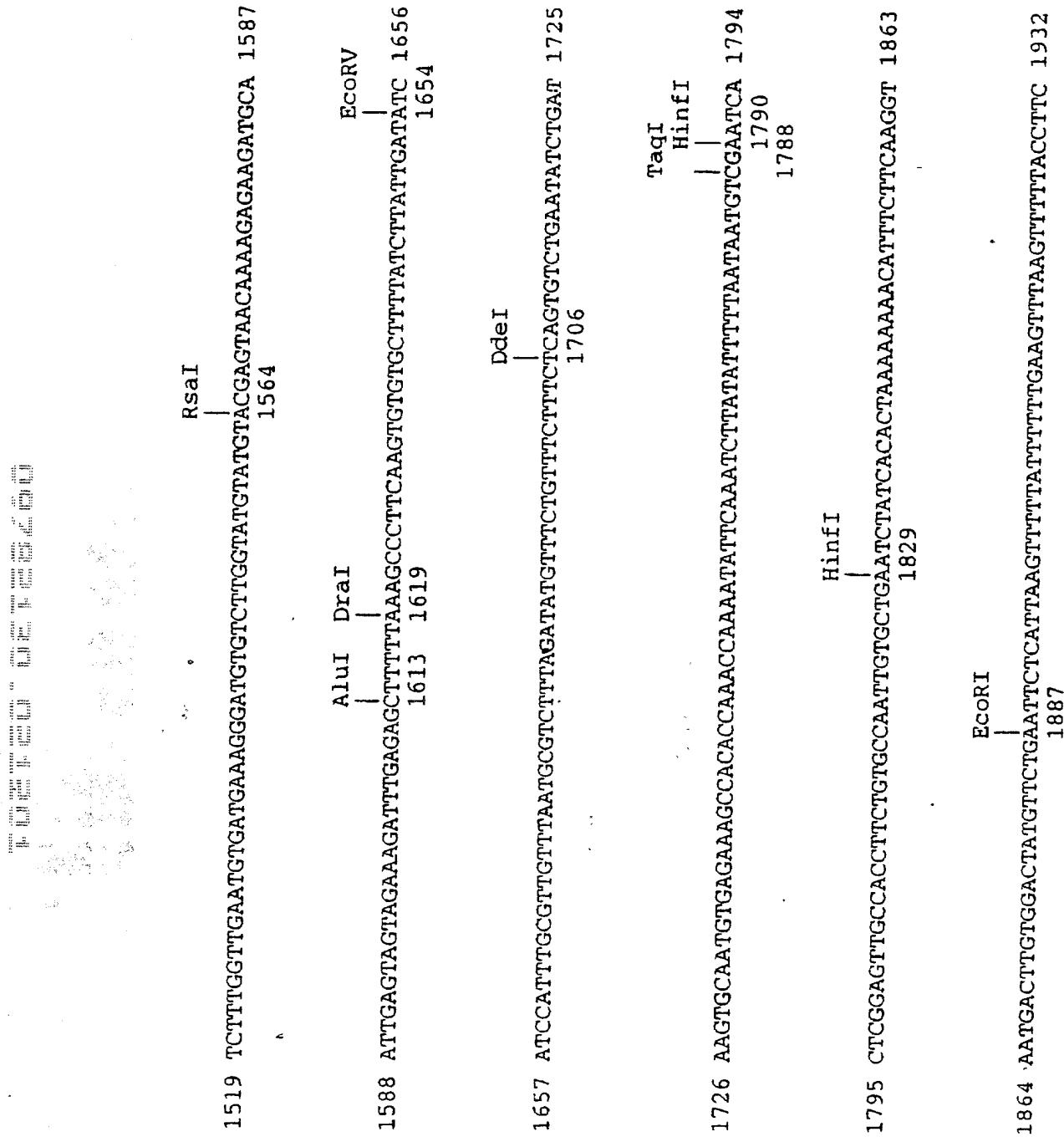
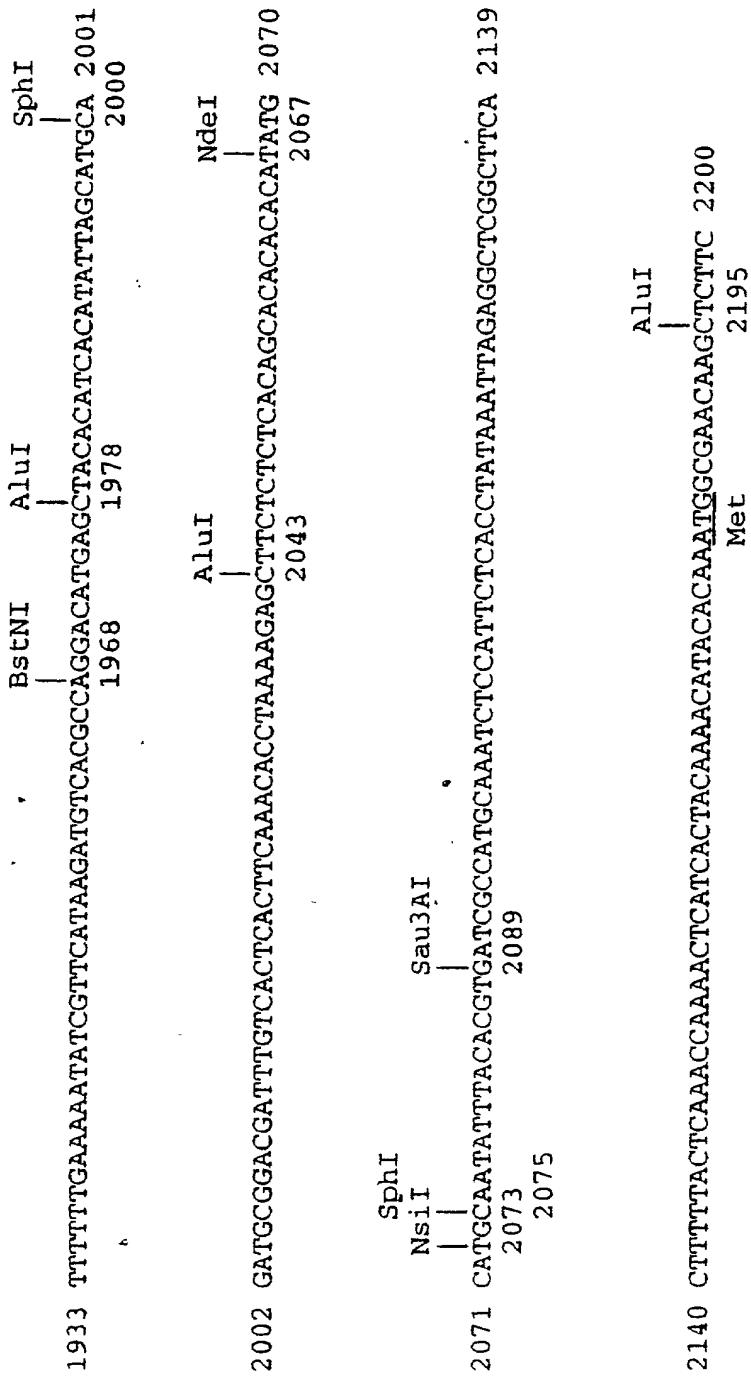


FIG. 1F



Lambda CGN1-2

Length = 4325
NCG-186 Linear

101

Aye

三

TCGAG

23

1

Xhai Xbai

70 ACTCTAATTGAGCCGTTCCTTAC

NOTES ON THE SUBCULTURE

85

CE
30

三

39 TTTCTTGTTCATA

150 ...CCTTCCTTAACTTGATTAATTCCTGAAAGTGCCTCTTTGGCAAA 207

20 / 150

206 08 TGTAGGTTGGCAAAACGAGGAACATTCCTTCTCCCTT

276
Sau3AI

SAU3AI
ddel

'7 TAAGAAATAGGCAAGTCCTTGCTTACCTGAACTT

...GAGGATCAGCTATAACGGTCGTCGCCATGAAAACCC

309 345
TGT GCG TCC CCA GAA ACAGAGGT

305

346 AAAACATTTCATACACTTGAAGTTCTCACTAATCTGTAAATCTTTGGTAGATATCACTA 414

FIG. 2A

FIG. 2B

HincII
HhaI
HaeIII
DdeI
BstEII
BaiI
AluI
HaeIII
AluI
415 CAATGTCGGAGAGACAA3GGCTGMNCANCATAACAAAAGGAAATGAAGATGGCCTTTGATTAGCTG 483
439
438
439
439
440
438

AluI
HinfI
484 TGTAGCATCAGCAGCTTAATCTCTGGGCTCTCATGGATGCTGGAAACTGGATTCAACTCTCAAAGTTA 552
498
535

MspI
HpaII
HinfI
553 TGAGTTGTCACCGGTCTCTACACAGGTAAATAATCAGTTGAAGCAATTAAAGAACATTGATTGT 621
564
564
Pdel
564

622 AGTAAACTAAGAAGAACTTACCTTAIGTTTCCCCGCAGGACIGGATTATGGAACAAIGGGAAAGAAC 690
629

AluI
AluI
SacI
AluI
691 TACTATAAAGCTCCATAGCTGGTTCAAGATAACGGGAAGCTCTTAGTTGTTATGTCAAAAGGTTAGTGT 759
702
710
729
731

760 TTATGTAAATAAAGCTTATACCAACAAAGTCCTCATTTGACTTATTAATCCTTGTGAAATTGCTAG 828
 PstI
 829 GAACTACTTATTC|CAGCGAGTCATACAAAGTGAGGAGCTCATTTCCGTCAAGGGATAAAATTAAGAA 897
 842
 865

$\left[\begin{matrix} \text{XbaI} \\ \text{BclI} \end{matrix} \right]$

898 GGAAAGAAGAATTTCAGTACGGTAAAGCTTACATGAACTGGTAAICGTTGGGGTGCGGAAATGTCGAGGA 966
 908

$\left[\begin{matrix} \text{Sau3A} \\ \text{Bpu1} \end{matrix} \right]$

967 ACTCTGGCTTCTCTGATCAGGTAGGGTTTTCGCTTAACTTGTCTGGGTTTTTATTCCTCCCTGATG 1035
 981

$\left[\begin{matrix} \text{AluI} \\ \text{RsaI} \end{matrix} \right]$

1036 CTATAATGATAAACTCTGGCTTCTGGGTTTGGACTTTTGTACCCAGGGATTCAC 1044
 1074 1087

1105 ATAGGAGGTGGGAGAAAGGGTAAAGGAAATACATCAAGGAGAACATGGCAACTGGGATCAAGGAGCTTTCATAT 1173
 1155 1165

$\left[\begin{matrix} \text{Sau3A} \\ \text{AluI} \end{matrix} \right]$

1174 TTAGGCAATCCAAAGCTTAAGATGGGGATGAAACTCAAGGGAGCTCTGGACCAACCCCTTCAGGA 1242
 1215

$\left[\begin{matrix} \text{HinfI} \\ \text{RsaI} \end{matrix} \right]$

1242

FIG. 2C

1243	CTCATGTCAGGTGGTTCTTAGCTTGAACACAGATTGGATCTTTGGTTCATATACT	<u>BpuI</u>	Sau3AI	<u>BpuI</u>
		<u>BpuI</u>	<u>BpuI</u>	<u>BpuI</u>
1268		1285		1311
1312	TAGGACCTGAGAGCTTTGGTGTGATTTCAGGACAAATGGCGAAGAACATTGTCATCA	<u>BpuI</u>	<u>HinfI</u>	<u>BpuI</u>
1315	1325		1363	1370
1319				
1381	ATATGCTATGGCAGGACAGTGTGCTGATAACACACTTAAGCATCATGTGGAAAGACAATTGGAG	<u>HinfI</u>	<u>HinfI</u>	1449
1450	CGAGACTCAGGGTCTGATTAACCAATCAAAGACGTAAAACCAGACGCAACCTCTTGGTGAATGTA	<u>BpuI</u>	<u>BpuI</u>	1518
1454				
1456				
1519	ATGAAAGGGATGTCCTGGTATGTATGTCGAATAACAAAAGAGAGATGGAAATTAGTAGTAAATA	<u>BpuI</u>	<u>BpuI</u>	1587
1548				
1588	TTTGGGAGCTTTAAGCCCTCAAGGTGGCTTTTAACTGATCATCCATTGGTTTAA	<u>BpuI</u>	<u>EcoRV</u>	1656
1596				
1635				
1664	TGGCTCTAGATATGTTCTATCTTCTCAGTGTCTGATAAGTGAAATGAGAAAACATACCAA	<u>XbaI</u>	<u>BpuI</u>	1725
1687				

2209	AAT GCT CCG GTC TAC AGG AC GG TT GTGGAAAGT GATGCCACAAAATCCAGGGCCATT Asn Thr Val Pro Lys Ser Val	HinfI	TaqI	NaeI
			AccI	MspI
			SalI	HpaI
			HincII	HaeIII
2277	AAT GCT CCG GTC TAC AGG AC GG TT GTGGAAAGT GATGCCACAAAATCCAGGGCCATT Arg Prol Lys Ser Val	HinfI	TaqI	NaeI
			AccI	MspI
			SalI	HpaI
			HincII	HaeIII
2278	AGG ATTC AAA ATT GGG AAG GAG GTT CAGCAGGACACACCTGAAGCTGGCCACAAATGGCTCCAC Arg Prol Lys Ser Val	HinfI	TaqI	NaeI
			AccI	MspI
			SalI	HpaI
			HincII	HaeIII
2346	AGG ATTC AAA ATT GGG AAG GAG GTT CAGCAGGACACACCTGAAGCTGGCCACAAATGGCTCCAC Arg Prol Lys Ser Val	HinfI	TaqI	NaeI
			AccI	MspI
			SalI	HpaI
			HincII	HaeIII
2415	AGG ATTC AAA ATT GGG AAG GAG GTT CAGCAGGACACACCTGAAGCTGGCCACAAATGGCTCCAC Val Lys Ser Val	HinfI	TaqI	NaeI
			AccI	MspI
			SalI	HpaI
			HincII	HaeIII
2484	GTT GAG AAC ACA AAC AGG CCC ACC AGG AGG CC ACC GGT GCT CAG GAG TGC AAC GAG ATT Val Lys Ser Val	HinfI	TaqI	NaeI
			AccI	MspI
			SalI	HpaI
			HincII	HaeIII
2485	CAG GAG AGC CAC TT GGG TT TGC C AAC CTG AGG AGC AAC CAAG CGT TAA CAAC AGA ATT Gly Pro Leu Cys Val Cys Pro Thr Lys Glu Asp Val Lys Glu Val Lys Glu	HinfI	TaqI	NaeI
			AccI	MspI
			SalI	HpaI
			HincII	HaeIII

FIG. 2F

FIG. 2G

2968 CAGTCAGTTTCTTAATTGCTTAAGCTTCAAGGCCTTCAAGGTAGTAAAGATCATCCA 3016
 Sau3AI

3037 ATGGGATCCAACAAAGACTCAAATCIGGGTTGATCAGGACTCAAAACATTTGTTTCAATTAAA 3105
 3041 3053 3069 3069

3116 TTATGCAAGTGTCTTTAATTTGGTGAAAGACTTTAGAACAAAGAACGACAGGTTAATTTAAA 3174
 HinfI

3175 ACAAAGTTCAAGTATTAGATTTTGACTTATTTGCTTATGTTGAAAGTTGAGGTTGAGAACATTAAATGATACTGTCACATATCCAA 3243
 3135

3244 GTTTTATTTATATATGCTTGTCTTCAAGGTTGAGATTGAGAACATTAAATGATACTGTCACATATCCAA 3312
 NdeI

3313 TATTTTATGTTTCAATTGCTGTTCAACATATGATAAGATGGTCAAATGTTGAGTTGTTGTTTAC 3381
 3341

3382 CTGAAGAAAGATAAGGAGCTTCTGAGTTCTGAAGGGTACGTCACTTCACTTCTGGCTAAAGCGA 3450
 AluI TaqI

3402 3405 3421 3425

3451 ATATGACATCACCAAGAAAGCCGAAWAGGAAACTCTGGCTTAAACCA 3519 FIG. 2H

FIG. 21

3934 TCGAATCTTAACTTGTGTTACCGATAAACCTTAAAGCTTAAAGCTTAAAGTCATA 4002
 3935 AluI HindIII PstI
 3937 XbaI HinfI PstI
 3938 GCTTGAACTGGAACTGGCTTCTGCTTAAAGTGTCCCTTTGAGTGTCACTGCTTA 4071
 4000 HinfI HinfI PstI
 4004 HinfI HinfI PstI
 4006 HinfI HinfI PstI
 4021 HinfI HinfI PstI
 4059 HinfI HinfI PstI
 4069 HinfI HinfI PstI
 4072 GCACCTTGTAGATTCACTTGTGTTAAAGTAAAGGTAAGAACCTTGGACTTCTCCCGTTATG 4140
 4141 ACAAGGTTAACCTTGTGGTTAAACAGAGTGGACCTTCTCAGCTTGGGGCTGGCTGG 4209
 4146 HincII HincII Sau3AI
 4147 HincII HincII Sau3AI
 4148 HincII HincII Sau3AI
 4149 HincII HincII Sau3AI
 4150 HincII HincII Sau3AI
 4210 GACCAAGCTCTCAGGGAAATCCCTACTCAATGCCCAAATCTACTGGAAAAGACACAGAT 4278
 4210 HincII HincII Sau3AI
 4211 HincII HincII Sau3AI
 4212 HincII HincII Sau3AI
 4213 HincII HincII Sau3AI
 4214 HincII HincII Sau3AI
 4215 HincII HincII Sau3AI
 4216 HincII HincII Sau3AI
 4217 HincII HincII Sau3AI
 4222 HincII HincII Sau3AI
 4231 HincII HincII Sau3AI
 4294 HincII HincII Sau3AI
 4300 HincII HincII Sau3AI
 4316 HincII HincII Sau3AI
 4321 HincII HincII Sau3AI
 4325 HincII HincII Sau3AI
 4326 HincII HincII Sau3AI
 4327 HincII HincII Sau3AI
 4328 HincII HincII Sau3AI
 4329 HincII HincII Sau3AI
 4330 HincII HincII Sau3AI
 4331 HincII HincII Sau3AI
 4332 HincII HincII Sau3AI
 4333 HincII HincII Sau3AI
 4334 HincII HincII Sau3AI
 4335 HincII HincII Sau3AI

FIG. 2J

Brassica campestris ACP Genomic Sequence

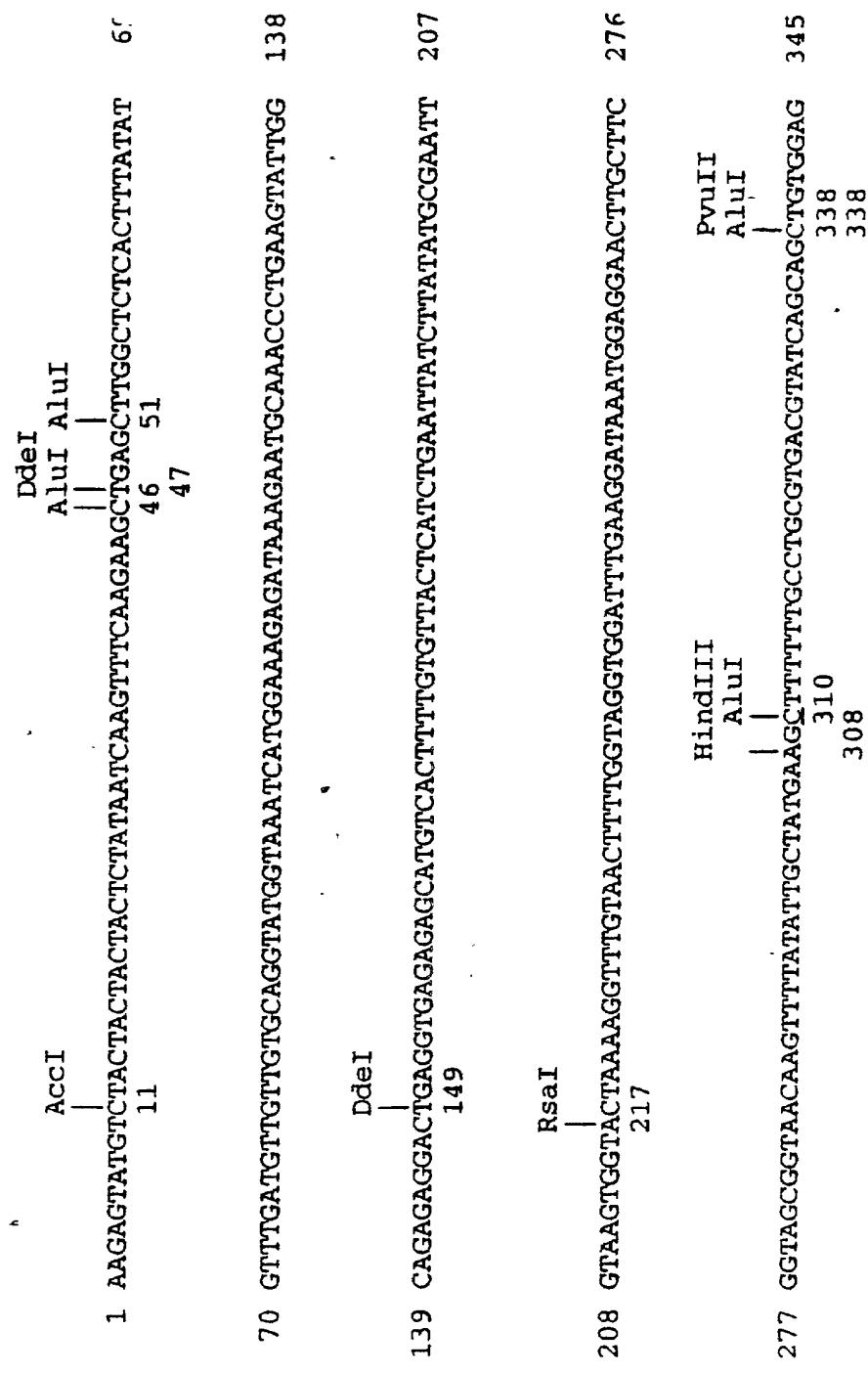


FIG. 3A

FIG. 3B

<p>346 AAGATGGTATTAGAAAGGGCTTTACATTTGTGACAATAATTAAATTGGCCGGTATGGTTT 414</p> <p style="text-align: center;">MspI HpaII HaeIII</p> <p style="text-align: center;">403 404 404</p>	<p>415 GGTTAAGACTTGTGAGAGACGTGTGGGGTTTTGATGTATAATTAGTCGTGTTAGAACCAA 483</p> <p style="text-align: center;">Tth111I 552</p> <p style="text-align: center;">547</p>	<p>484 GACTTGTTGNGTATGCTTTTAACCTGAGGGGGTTCTGTGTTAGTTAGGAACCTTGACTTGCT 592</p> <p style="text-align: center;">Sau3AI BglII RsaI</p> <p style="text-align: center;">564 593 564 593</p>	<p>553 CTTTCTCAAGATACTGATTGGTAAGGGCTGGCTGGTAGCTACTGTTGGTTAATTGGTTTGACTATT 621</p> <p style="text-align: center;">HinfI HaeIII DraI</p> <p style="text-align: center;">623 634 646</p>	<p>622 GAGTCACTGTGGCCCATTGACTTTAATTAGGCTGGTATAATTGGCTGGTTAAAACCGGTCTGAGATAAG 690</p> <p style="text-align: center;">HpaII DraI MspI DdeI 673 678 683 678</p>
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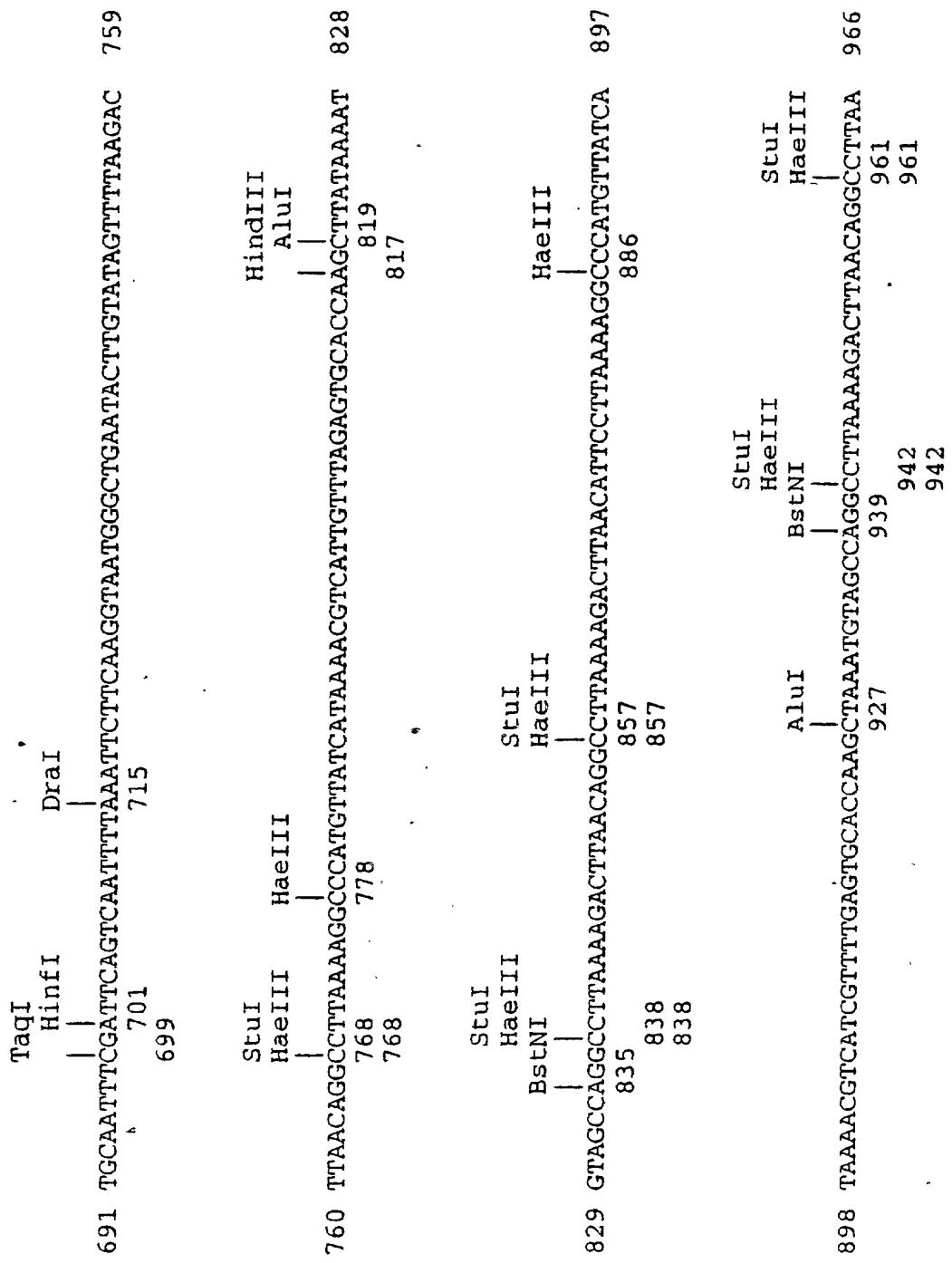


FIG. 3C

967 AAGGCCATCATATAAACGCCCGTCGTTTGAGTGCACCAAGCTTATAAAATGTAGCCAGCTACCTC 1035
 971 1012 1029 1034
 1010

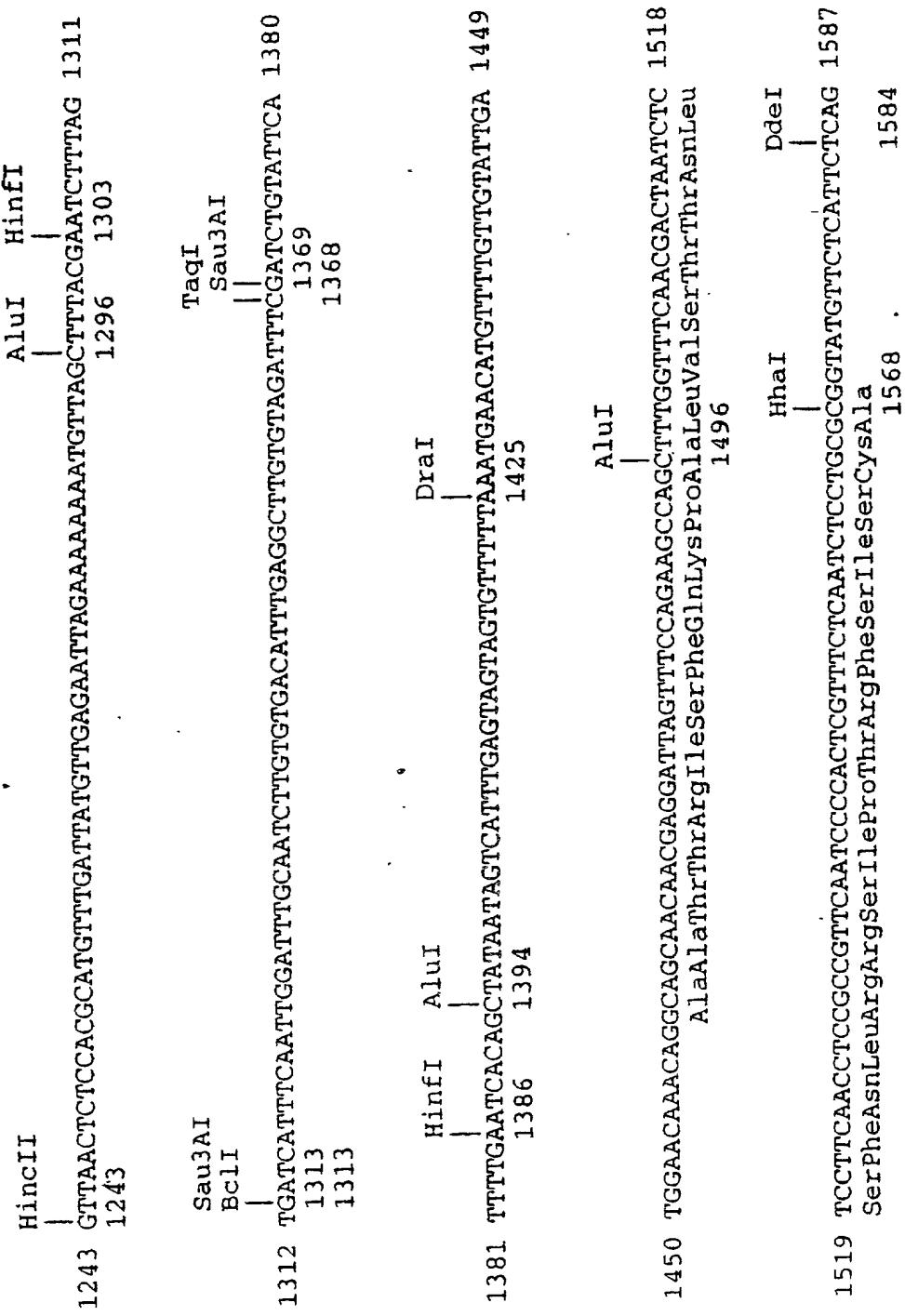
HindIII
 HaeIII
 AluI
 AluI AvaiI
 |
 1036 GGGACATCACGCTCTTGTACACTCCGCCATCTCTCTCTCGAGCAGATCTCTCGGGAAATATCG 1104
 1055 1078 1085 1093 1103
 1079 1085
 1078

XbaI
 TaqI
 AvaiI
 Sau3AI
 BglII
 AvaiI
 TaqI
 |
 1105 ACAATGTCGACCACCTTCTGCTCTCGTCTCCATGCAAGGCCACTCTGGTAATCTCATCTCCTCT 1173
 METSerThrPheCysSerValSerMetGlnAlaThrSerLeu
 1112
 1110
 1111
 1112
 1108

Tth11II
 TaqI
 SalI
 HincII
 AccI
 |
 1174 TGTGTTCCAGATCGCTCTGATCATACCTTCTGATTCATTAGATCATTGGCTCTGATCTGTTGATGTT 1242
 1184 1193 1210 1224
 1193

FIG. 3D

FIG. 3E



TaqI	AluI	RsaI	HaeIII
1588 CATTATTTCCAGCTTGTCTGGTACTCTTAATTGTTATTGGTTATTAGGCCAACCAACAG 1656			
1597 1601 1616 1648	DdeI	AluI	AlaLysProG
1657 AGACGGTTGAGAAAAGTAGTTAAGATAAGTCTAACTCAAAGACGCCAAAGGTCGTTG 1725			
lufThrValGluLysValSerLysValLeuSerLysGlnLeuSerLeuAspGlnLysValValA 1695			
1676			
Sau3A I	HinfI	TaqI	
1726 CGGAGACCAAGTTTGCTGATCTGGAGCAGATTCTCGACACTGTAAGTCATCAATCATTTCTATG 1794			
laGluThrLysPheAlaAspLeuGlyAlaAspSerLeuAspThr 1743 1756 1763			
1795 TGAATAAAGAGAACTTGAAGAGTTTGTTAACATATTAACTGAGTGTGTTGCATGCAGGTTGAGATA 1863	DdeI	SphI	
ValMetGlyLeuGluGluGluPheAspIleGluLysMetAlaGluGluLysValGluIleAlaThrVal 1891 1893			ValGluIle
1891 1893			
TaqI	DdeI		
ECORV	AluI		
1864 GTGATGGGTTAGAGGAAGAGTTGATATCGAAATGGCTGAAGAGAAAGCTCAGAGATTGCTACTGTC 1932			
ValMetGlyLeuGluGluGluPheAspIleGluLysMetAlaGluGluLysValGluIleAlaThrVal 1913 1914			
1913 1914			

FIG. 3 E

FIG. 3G

1911 GAGGAAGCTGGCTGAACTCATTGAAGAGCTCCCTCAACTTAAGAACTTAATTTAGTATTAAAGGAGCCA 2001
AluI |
GluGluAlaAlaGluLeuIleGluGluLeuValGlnLeuLys
1940 1960 1962

2002 AGGCTTGTGGGTTGTTCTATAATCTCCTGCTTCATTTCCTTAAATGTCAGCGAAC 2070
SacI |
AluI |

2071 TCTGGTTAAAGTAGTATCTGGTTCGCCATGGATCTCTCTATTCGACTGAAAGCTTGCTT 2139
BpuI |
2082

2100 2104 2119 2121 2120 2121

2140 TACACATGAAAGCTP 2154
HindIII |
AluI |
2152 2150

TaqI |
Sau3AI |
SalI |
HincII |
AccI |||
2121

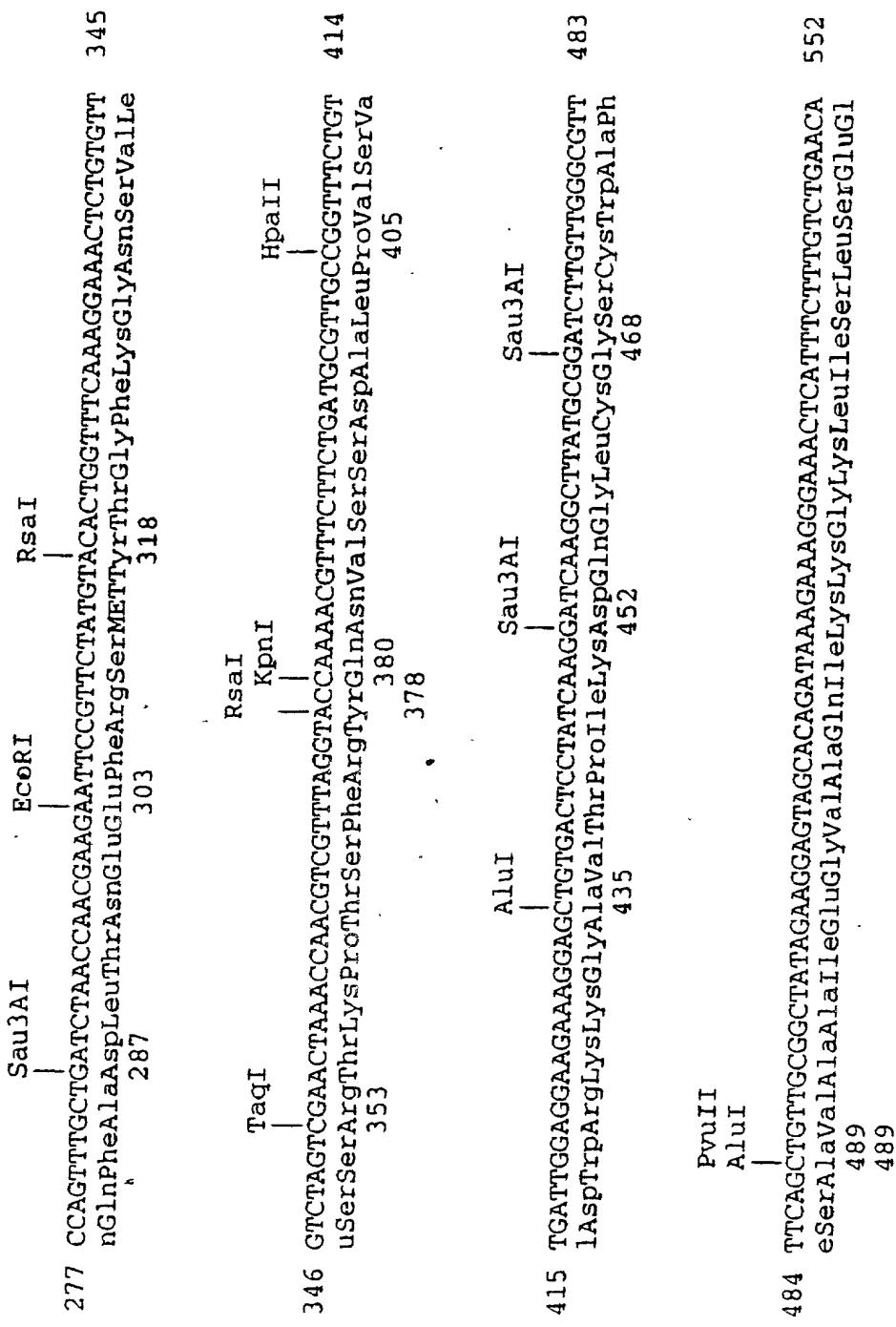
Brassica Campestris Seed Specific cDNA-EA9

<pre> 1 TTCAACTTTCTAAACCAAAATGGCTTAACACAGATCCAAATCTTCTCATTTGTCATC METAlaLeuThrGlnIleGlnIlePheLeuIleValSerLeuValSerSe 34 </pre>	<pre> Sau3AI TagI Sau3AI ClaI TagI TagI 70 ATTCAAGTTATCGATCACTCTCGTCCATTACTCGATGAAGTGCCTACGCCATGCCGA rPheSerLeuSerIleThrLeuSerArgProLeuLeuAspGluValAlaMetGlnLysArgHisAlaG1 81 82 81 </pre>	<pre> HaeIII 139 GTGGGATGACCGAACACGGCCGTGTTACGGCAGATGCGAACGAGAAAAACAAACCGCTACGCCATGCCGA UTTPMETrGluHisGlyArgValTyralaAspAlaAsnGluLysAsnAsnArgTyraIlaValPhely 157 </pre>	<pre> HpaII 208 ACGCAACGTGGAACGGCATTGAAACGGCTTAATGACGGTTCAATGCCGACTAACGTTAACCTCGGGTGA sArgAsnValGluArgIleGluArgLeuAsnAspValGlnSerGlyLeuThrPhelysLeuAlaValAs 250 263 </pre>	<pre> DraI 207 </pre>
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Complete nucleotide sequence of *B. campestris* cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of the sequence and a potential polyadenylation signal is underlined.

FIG. 4A

FIG. 4B



TagI
 Sall
 HincII
 AluI AccI
 |||
 553 AGAGCTTGTCGACTGGACACAAACGATGGTGGCATGGCGGTTGATGGATAACAGCGTTAACTA
 nGluLeuValAspCysAspThrAsnAspGlyGlyCysMetGlyLeuMetAspThrAlaPheAsnTy
 557 562
 560
 561
 562

622 CACAATAACTATTGGGGCTAACCTCTGAATTATCCTTATAAAGCACAAACGGCACTTGCAA
 rThrIleThrIleGlyGlyLeuThrSerGluSerAsnTyProtYrSerThrAsnGlyThrCysAs
 HpaII

691 CTTCAATAACAGATAAGCAACTTCTATCAAAGGTCTTGAGGATGTCGGCTAACGATGAGAA
 nPheAsnLysThrLysGlnIleAlaThrSerIleLysGlyLeuAspValProAlaAsnAspGlyL
 744

HpaII

760 AGCCCTAATGAAGGCCAGTGGCACACCCGGTAGCATGGAAATAGGGGAGGAGATATTGGTTCCA
 SAIAleUmetLysAlaValAlaHisProValSerIleAlaGlyGlyAspIleGlyPheGly
 789

Sau3AI
 HpaII
 BcII

829 ATTCTATTCGTCGGGCGTCAGGGAGAATGCAACTCATCTGTTGACGGGTTAACATGCGGTTGG
 nPhetyrSerGlyValPheSerGlyGluCysThrHisLeuAspHisGlyValThrAlaValG
 841
 875
 875

FIG. 4C

FIG. 4D

<pre> ScaI Sau3AI HaeIII RsaI 898 ATACGGCCGATCTAAACGGATTAAAGTACTGGATCCTCAAGAATTCATGGGGACCAAATGGGAGA 966 YTyrgLysArgSerlysAsnGlyLeuLysTyrTrpIleLeuLysProlysTrpGlyProlysTrpGlyG1 904 931 941 951 906 927 931 927 </pre>	<pre> Sau3AI EcorI BamHI EcorI 967 ACGTGGATACATGAGGATCAAAAAGATAATCAAGCCTAAACACGGACAATGTGGCTTGCATGAATGC 1035 uArgGlyTyrMetArgIleLysAspIleLysProlysProlysHisGlyGlnCysGlyLeuAlaMETasnAl 982 995 </pre>	<pre> Sau3AI EcorV 1036 TTTCGTACCCAACTATGTGAAAAAAATCGGTTCAAAATATCGGTTAAGCTTTAGAATAAATGTTGTTGG 1104 aSerTyrProThrMet 1041 </pre>	<pre> RsaI HindIII HpaII AluI 1105 TTATAATTAAAGACTCTGTTGCATGTAATTGTGAAATGGTAAGTTATGTGATGCAAAAGATTGATA 1173 </pre>	<pre> 1174 AAAAAAAA 1186 </pre>
--	---	--	--	---------------------------------

3H11 TTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA 51

3H11 GCTTACAGCTGGGAGAACATTGTCACTCTCTGAAATTAAATGTTATC 102

3H11 CAGAATCCTTCATCATAAAATAATCAAAATGCAAATCTATTTTCTAC 153

3H11 TCTTGTCTAGCTCAACTTCTTCTGCTCATCAATTAGCAATTAATCC 204
TGCTCATCAATTAGCAATTAATCC

3H11 AAAACCATTATGGCTGCCAAAAATTCAAGAGATGAAGTTGCTATCTTCTTC 255

2A11 AAAACCATTATGGCTGCCAAAAATTCAAGAGATGAAGTTGCTATCTTCTTC
METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe

3H11 GTTGTCTTTGACGACCACTTAGTTGATATGTCTGGAATTTCGAAAATG 306

2A11 GTTGTCTTTGACGACCACTTAGTTGATATGTCTGGAATTTCGAAAATG
ValValLeuLeuThrThrLeuValAspMETSerGlyIleSerLysMET

3H11 CAAGTGATGGCTCTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG 357

2A11 CAAGTGATGGCTCTCGAGACATACCCCCACAAGAAACATTGCTGAAAATG
GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET

3H11 AAGCTACTTCCCACAAATATTTGGACTTGTAAACGAACCTTGCAGCTCA 408

2A11 AAGCTACTTCCCACAAATATTTGGACTTGTAAACGAACCTTGCAGCTCA
LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer

3H11 AACTCTGATTGCATCGGAATTACCCCTTGCCATTGGTAAGGAGAACAGC 459

2A11 AACTCTGATTGCATCGGAATTACCCCTTGCCATTGGTAAGGAGAACAGC
AsnSerAspCysIleGlyIleThrLeuCysGlnPheCysLysGluLysThr

3H11 GACCAGTATGGTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA 510

2A11 GACCAGTATGGTTAACATACCGTACATGCAACCTGTTGCCTTGAACAATA
AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro

FIGURE 5A

3H11 TCAATGATCTATCGATCGATCTATCTATCTATTATCTGTCTCGCGCTA 561
2A11 TCAATGATCTATCGATCGATCTATCTATCTATTATCTGTCTCGCGCTA

3H11 TAGTGTGTCGTACCTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612
2A11 TAGTGTGTCGTACCTTGGTGTGAAGAATATGAATAAAGGGATACATAT

3H11 ATCTAGATATATTCTAGGTAATGTCTATTGTATTAAAATTGTAGCAAT 663
2A11 ATCTAGATATATTCTAGGTAATGTCTATTGTATTAAAATTGTAGCAAT

3H11 GATTGTTGAATAAAACATACCATGAGTGAAATAATTATTCCACATTAAT 714
2A11 GATTGTTGAATAAAACATACCATGAGTGAAATAATTATTCC

3H11 TCACGTATTTATTCACTTATGATACGTATTTGTTCCCTTCGCGTAAAA 765

3H11 AAAAAAAA 774

FIGURE 5B

2A11	⑤M A L R D I P P Q E T L L
PAlb	⑤C S P F D I P P C G S P L C R C I
Chick pea inhibitor	⑤C T - K S I P P - - - Q C R C N
Lima bean inhibitor	L C T - K S I P P - - - Q C R C T
α_1 -antitrypsin	L G A I P M S I P P E V

2A11	T N I L G L C N E P C S S N S D C I
PAlb	G S P L C R C I P A G L V I G N C R
Barley chloroform/ methanol-soluble protein d	T N L L G N C R - F Y L V Q Q T C A
Wheat α -amylase inhibitor 0.28	V S A L T G C R - A M V K L Q - C V
Wheat albumin	V P A L P A C R P L - L R L Q - C N
Millet bi-functional inhibitor	N N P L D S C R W Y V S A T E R . T C G
Castor bean 2S small subunit	Q Q N I L R Q C Q E Y I K Q Q V S G Q
Napin small subunit	A Q N I L R A C Q Q W L N K Q A M Q S

FIGURE 6

2A11 GENOM.

	10	20	30	40	50
CTCGAGCCCT	TTAAAAAGTA	TAGTCAATAT	TTACGGTGAC	CGTGAATTTC	
60	70	80	90	100	
TTAATTATGA	TATATAATTT	AAAAGAAATC	ATGATCACAT	TCTACTGATG	
110	120	130	140	150	
AGAACATGTG	CTAATCAAGG	GAAAACATGG	ATGTGAAAAAA	TACTTTTGT	
160	170	180	190	200	
TAAAAGTAAA	AAAAAAATGTG	AAATTTGTT	AGTTATTAC	TACCTATACA	
210	220	230	240	250	
TTATTTGAGC	ATGTGCAAAC	TTTACAAATA	CCTAATAGAA	GATTTTCACC	
260	270	280	290	300	
TGCCTGTATA	TATGTAATT	AATTATAATG	AACACTCTCA	CATAAAATAA	
310	320	330	340	350	
TTATCAGTAT	ATACATTAAT	ACTTGCCCTC	CACAATGAAT	TAAATAAAAT	
360	370	380	390	400	
GTAGAACATG	ATCTACACTT	CAATAAAACT	AAGACCATAA	AGAATAATT	
410	420	430	440	450	
CAAAATATAC	ACATGTCAAC	AATAAATTAT	TTGCATATTA	TATTAACCTA	
460	470	480	490	500	
CTAAACAAATC	TTTACTTTG	AAATATAAAA	ATAATCAAGT	TATAAGTCTG	
510	520	530	540	550	
CTCAAAGTAA	AGCACTTGT	AGACTCATCT	GATTTGAGA	AGGTAAGCAA	
560	570	580	590	600	
ATTGATGGTG	CATAATAGTC	ACAAGTAAAA	TATAAAATAG	ATTCATTAG	
610	620	630	640	650	
TAAAATTGTT	TTTACTTTC	TTTATATATA	ATTATCAATA	TCCTTCAATG	
660	670	680	690	700	
GTAGGTTAAT	TATATTGTTA	ACTTCTTGT	GAATTAAAGC	AATAAGACAA	
710	720	730	740	750	
GAATATTAAA	GATAAAAGAA	CAATAAAAT	AGAAAGACTA	AGAGATAAGA	
760	770	780	790	800	
GTTTCTTAT	TCTTCTTCA	ATAAGTATCA	TCAAGTGTAT	ACAATATAAA	
810	820	830	840	850	
TTTTTGTATT	TTTGATCTAT	CTATTTATAA	TGTTATATAT	AAGCATAACAA	
860	870	880	890	900	
AAGATCAGTC	ATAAAATATGA	CTTTAATCAT	GAAAATAATG	AAAGAGATTA	
910	920	930	940	950	
TGAAGGCGTA	AGGTTACTAG	AATAATAGTC	ATTAAAAAAA	GGGGTTATCT	
960	970	980	990	1000	
TTATAATTGA	ATAATTGATG	AAGTAATGGA	GATAATTAGT	GAGCATAAAAT	
1010	1020	1030	1040	1050	
TTTTTTAAAA	AAATGGACAT	TTACACTATA	ATATTTATA	ACACTTTCCC	
1060	1070	1080	1090	1100	
TTAAACATCT	AGGTATAAAAT	AATGAGTCTT	GTCAAAATCT	TAGTAGGAAA	

FIGURE 7A

1110	1120	1130	140	1150
AATTCTGTGA	AATTTTTTA	GTGAAAACAA	ATGATATAAA	TATCTTGAAT
1160	1170	1180	1190	1200
ACTCATTATT	TGTTGTCTCA	TTAAAAAATCT	TATCTGACCT	ATAAAATAAA
1210	1220	1230	1240	1250
TTATTTGCTC	AACTCAAAAT	AGTTTTCAT	TCTAAAATT	GTATAATTAT
1260	1270	1280	1290	1300
TAGTGAATAT	TTAATTAACA	TAATTGTATA	CTAAGGGGCC	TATAAATTGG
1310	1320	1330	1340	1350
ATTCTTCTCA	AAGAAAAATA	AAATCACAC	ACAACTTTCT	TCTCTGCTC
1360	1370	1381	-1390	
ATCAATTAGC	AATTAATCCA	AAACCATT	ATG GCT GCC AAA AAT	
			MET Ala Ala Lys Asn	
1399	1408	1417	1426	
TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT CTT TTG				
Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val Leu Leu				
1435	1444	1454	1464	1474
ACG ACC ACT TTA GGTCACAAAC	ACTTCTCCCT	TATTTGT	TTT	
Thr Thr Thr Leu				
1484	1494	1504	1514	1524
TCTTAATTTC	TTGGAAGTCA	TATGCATGTG	TTTGGTATCA	TGGTATATAT
1534	1544	1554	1564	1574
ATAAAGGAAA	ATATTTTCT	TAATTACTGG	TTTTCTAAC	TTTGGTAGGT
1584	1594	1604	1614	1624
AATCGGAAAT	TATTATGAGA	TAATGAAC	TGCAAAGTCAT	TATTATATAA
1634	1644	1654	1664	1674
CTTTTTTTT	ATACTTGAT	TTAAGAAC	ATTTTCTCA	TTTTATATAA
1684	1694	1704	1714	1724
ACTTATTTT	CAACAGAAA	TATTTTCGA	ACTATTCAA	CACACCCTAA
1734	1744	1754	1764	1774
GACATTACAT	ATATATATAT	ATACACCCTC	CGTTTATAT	TACTTAATGC
1784	1794	1804	1814	1824
CTATTGAGTT	GGCCCACCC	TTAAGAATGA	TTCAATTAGA	GATATGTTT
1834	1844	1854	1864	1874
ACTAAATTAA	CCTATGCTTT	AAGACTCTAA	ATTGGCTAT	TACTATTTA
1884	1894	1904	1914	1924
CGTTGTAATT	TAATGACAAA	CATTTCTAA	TGACTATAGT	CTGAACCTAA
1934	1944	1954	1964	1974
TTAGACAGAC	GTATCTATAG	TTTGCTTACT	AATGATTCA	AGCTATATAT
1984	1994	2004	2014	2024
TTGGAGAGGA	GAGAGACAAA	CGATATTAG	AAAGGGAGGA	GAGAGGCGAG
2034	2044	2054	2064	2074
GTAAATCTGA	AATAGAGAAG	AGAAAGGCAA	CCAATTTGA	TCATCTATCA
2084	2094	2104	2114	2124
TACTTTGAT	TATTATTTT	ATTATATGTA	CGTTACATT	ACAGTTTCG

FIGURE 7B

2134	2144	2154	2164
AATTCTTACA	TTAATCTTAA	TCATAATATA	TACA
		GTT	GAT ATG
			Val Asp MET
2173	2182	2191	2200
TCT GGA ATT TCG AAA ATG CAA GTG ATG GCT CTT CGA GAC	Ser Gly Ile Ser Lys MET Gln Val MET Ala Leu Arg Asp		
2209	2218	2227	2236
ATA CCC CCA CAA GAA ACA TTG CTG AAA ATG AAG CTA CTT	Ile Pro Pro Gln Glu Thr Leu Leu Lys MET Lys Leu Leu		2245
2254	2263	2272	2281
CCC ACA AAT ATT TTG GGA CTT TGT AAC GAA CCT TGC AGC	Pro Thr Asn Ile Leu Gly Leu Cys Asn Glu Pro Cys Ser		
2290	2299	2308	2317
TCA AAC TCT GAT TGC ATC GGA ATT ACC CTT TGC CAA TTT	Ser Asn Ser Asp Cys Ile Gly Ile Thr Leu Cys Gln Phe		
2326	2335	2344	2353
TGT AAG GAG AAG ACG GAC CAG TAT GGT TTA ACA TAC CGT	Cys Lys Glu Lys Thr Asp Gln Tyr Gly Leu Thr Tyr Arg		2362
2371	2380	2393	2403
ACA TGC AAC CTG TTG CCT TGA ACAATATCAA TGATCTATCG	Thr Cys Asn Leu Leu Pro		
2413	2423	2433	2443
ATCGATCTAT CTATCTATTT ATCTGTCTCT GCGCGTATAG TGTTGTCTGT			2453
2463	2473	2483	2493
ACCTTTGGTG TGAAGAACAT GAATAAAGGG ATACATATAT CTAGATATAT			2503
2513	2523	2533	2543
TCTAGGTAAT GTCCTATTGT ATTTAAAATT TGTAGCAATG ATTGTTGAA			2553
2563	2573	2583	2593
TAAAAACATA CCATGAGTGA AATAATTATT CCACATTAAT TCACGTATTT			2603
2613	2623	2633	2643
ATTCACCTA TGATACGTAT TTTTGTTCCT TTCGCGTAGA TTTTTGATCC			2653
2663	2673	2683	2693
TTTTCCCTTT TGAATATTAA ACATTAACAA CAAATAATGT TTATTAAATT			2703
2713	2723	2733	2743
AAGTTAATAT TTTTATTAG CTATTTATAT TTTTATTTGA AATCAAACCTT			2753
2763	2773	2783	2793
GATAAAATATT TATAAAGATA ATTAACAAGT AATGTGACAC TAACACCATG			2803
2813	2823	2833	2843
TAATATTATC TTGTCGTTAT TTATGATAAT ATTTAAAAT TATAATTCA			2853
2863	2873	2883	2893
GTTAAAAAAAT TATTAAAAAA ACATACTTT AAAAAGTGAG TTAGCCTCCG			2903
2913	2923	2933	2943
CTACCCACAT ACTTATGAAT TGGACTAGTT GTTTTTGAC CCACAAAAAG			2953
2963	2973	2983	2993
AATGGGCTAA TTAAACCTGA CCTATCAAAT TTCAGAATCT GCATAGATTA			3003

FIGURE 7C

3013	3023	3033	3043	3053
GTCCGAACGA	AATGAGTCAG	CCCGTATTGA	ACAAAATATC	AACAAGGACG
3063	3073	3083	3093	3103
TTATGTAAAG	ATGTTAAGA	AGGAAAAAAAG	ATTTCTAATA	CATATGGACT
3113	3123	3133	3143	3153
TTCAATATCC	CAACTTTGTC	TGGCGATCTG	AACCCTGCTT	AGTTTGTGA
3163	3173	3183	3193	3203
TCATTAACCT	GTCTTGCTAT	GTATTTAAGA	TTTAAACTTT	ATATGTTAA
3213	3223	3233	3243	3253
ACTTACAGAA	AATACATATA	AATCTCTCAA	GACTTGGCAA	CATAATTTAC
3263	3273	3283	3293	3303
TTTAGTACTT	AAACTACATG	AAAATTAAA	TATCCTTTA	ACATCTTGA
3313	3323	3333	3343	3353
AGTGAATTAA	ATTATCACAA	TCCGAGCCTA	CACCTTGGAC	GTGGCCGGCA
3363	3373	3383	3393	3403
CTCAAGAACCC	AGTGCTGGTC	CCCAAGCTAA	CCCTCATCCT	GACTGACTAC
3413	3423	3433	3443	3453
AAGCGGAAGG	CTAACTTAAG	TATACAAAAG	CTTAAAAC TG	AATAAAAATAA
3463	3473	3483	3493	3503
ACTTTACAAG	GT TTTAACAC	AAATGAACAA	CTTTGAAGAA	AATAATATAT
3513	3523	3533	3543	3553
- TCAACTAGCC	ATAAAATAGA	CAACTTTAGT	CTTTAAAACA	TTTAATAAAA
3563	3573	3583	3593	3603
TAAATGC AAA	ATATAGACTC	CTTAACTAAA	CTGACTATCT	ATGGAGCCTC
3613	3623	3633	3643	3653
TAATTGATAA	AGATGGAAGT	CGGGACAAGA	CCACGACATC	CTGACTAAAC
3663	3673	3683	3693	3703
TGAGAAGTAA	ATAAAATCCC	CCGGAAAAAA	AGGAGCCTCA	CCATGGCTAA
3713	3723	3733	3743	3753
CTCGAACTCG	GGGATATATC	AATGAAGCTC	CTGTTGATGA	TCTTGAAGAC
3763	3773	3783	3793	3803
ATGTCTCTGC	ATCATCAAAA	AGATGCAGGC	CAAATGGCTC	AGTACGTAAA
3813	3823	3833	3843	3853
ATGTACGAGT	ATGTAAGGGA	AATTCTAAAG	TATAACATAA	GCTTGATACT
3863	3873	3883	3893	3903
TGAATAAAAG	GAAACATACT	TACCTCTTT	CAACTCAACT	CAAATTAAGA
3913	3923	3933	3943	3953
ATAAGATACT	CAACTCAAAG	ATTAGGTATT	CAACGCAAAT	ATGGCACTCT
3963	3973	3983	3993	4003
ACTCAATGAA	GTACAAATTA	ACTCAGGATA	CTCGACTTAA	GATACTCAAC
4013	4023	4033	4043	4053
TCCCGACACT	CAACTGAAC T	CATTTCAATA	TAAAGCAGCT	AAAAACAAGT
4063	4073	4083	4093	4103
TCAGTATAAA	GTAAAGTTGT	TTAAAAACAT	GATGTCAACT	CTGTGTGTAT
4113	4123	4133	4143	4153
AATAAGGGAT	ACAACATAAC	TTTGAAATGT	ATATAAAAAT	ACAATTAAC T

FIGURE 7D

416	4173	4183	4193	4203
GATGTATATA	AAAATACATT	AATCTATGGG	AGATTCTCTA	ACCGACAACC
4213	4223	4233	4243	4253
ATCACTTAAG	GGCTAAGATG	ATGATATAGC	GATCTACCGC	ACGCTGCCAT
4263	4273	4283	4293	4303
CGCATCTTAT	ACCCGGCCAA	AGGTATAAGA	CCTGAACCTGC	CTAATGAATC
4313	4323	4333	4343	4353
CACTAATAAA	CTGTTAAAAG	GAATCATCTA	AAAAGTATGA	CCCTTTCTA
4363	4373	4383	4393	4403
CCCATAGTGG	CTAACATGGT	TTATGGGGGC	TGTGAGTTAT	CTGAACCTCTC
4413	4423	4433	4443	4453
CCCCATATCG	GTGCTCAATA	CTACTCCAAA	AAATATACTG	CTCTTATGTT
4463	4473	4483	4493	4503
TAAAAACATA	CTGATTCTGT	GGTTTGAAAT	TATTGCTTAA	AGCTTAGATT
4513	4523	4533	4543	4553
TTTGAAAAGC	TCTCTTTGA	AAATCGTAGT	TTCCCTTTTC	TTCTATTAAA
4563	4573	4583	4593	4603
GCTAGACATA	GGCTATGTAG	AACTCTAGCT	TACCTCCCTT	CTCAAAAGTT
4613	4623	4633	4643	4653
TGAAAACATT	TGCTTAGATT	CTTAGGGACT	ACTTAGTTCC	CTTGTGGAA
	TTC			

FIGURE 7E

PG GENOMIC

10 20 30 40 50
AAGCTTCTTA AAAAGGCAAA TTGATTAATT TGAAGTCAAA ATAATTAATT

60 70 80 90 100
ATAACAGTGG TAAAGCACCT TAAGAAACCA TAGTTGAAA GGTTACCAAT

110 120 130 140 150
GCGCTATATA TTAATCAACT TGATAATATA AAAAAAAATT CAATTGAAA

160 170 180 190 200
AGGGCCTAAA ATATTCTCAA AGTATTGAA ATGGTACAAA ACTACCATCC

210 220 230 240 250
GTCCACCTAT TGACTCCAAA ATAAAATTAT TATCCACCTT TGAGTTAAA

260 270 280 290 300
ATTGACTACT TATATAACAA TTCTAAATT AAACATTTTT AATACTTTA

310 320 330 340 350
AAAATACATG GCGTTCAAAT ATTTAATATA ATTTAATTAA TGAATATCAT

360 370 380 390 400
TTATAAACCA ACCAACTACC AACTCATTA TCATTAATC CCACCCAAAT

410 420 430 440 450
TCTACTATCA AAATTGTCCT AACACTACT AAAACAAGAC GAAATTGTT

460 470 480 490 500
GAGTCGAAT CGAAGCACCA ATCTAATTAA GGTTGAGCCG CATATTTAGG

510 520 530 540 550
AGGACACTTT CAATAGTATT TTTTCAAGC ATGAATTGA AATTAAAGAT

560 570 580 590 600
TAATGGTAAA GAAGTAGTAC ATCCCGAATT AATTCAATGCC TTTTTTAAAT

610 620 630 640 650
ATAATTATAT AAATATTAT GATTTGTTT AAATATTAAA ACTTGAATAT

660 670 680 690 700
ATTATTTTT TAAAAATTAT CTATTAAGTA CCATCACATA ATTGAGACGA

710 720 730 740 750
AGGAATAATT AAGATGAACA TAGTGTTAA TTAGTAATGG ATGGGTAGTA

FIGURE 8A

760 770 780 790 800
AATTTATTAA TAAATTATAT CAATAAGTTA AATTATAACA AATATTTGAG

810 820 830 840 850
CGCCATGTAT TTTAAAAAAAT ATTAAATAGT TTGAATTTAA AACCGTTAGA

860 870 880 890 900
TAAATGGTCA ATTTTGAACC CAAAAGTGGTA TGAGAAGGGT ATTTTAGAGC

910 920 930 940 950
CAATAGGRGG ATGAGAAGGA TATTTGAAG CCAATATGTG ATGGATGAAG

960 970 980 990 1000
GATAATTTG TATCATTCT AATACTTTAA AGATATTTA GGTCACTTC

1010 1020 1030 1040 1050
CCTTCTTTAG TTTATAGACT ATAGTGTAG TTCATCGAAT ATCATCTATT

1060 1070 1080 1090 1100
ATTTCCGTCT TAAATTATTT TTTATTTAT AAATTTTTA AAAATAAATT

1110 1120 1130 1140 1150
ATTTTTCCA TTTAACCTTG ATTGTAATTA ATTTTAAAAA ATTACCAACA

1160 1170 1180 1190 1200
TATAAATAAA ATTAATATTT AACAAAGAAT TGTAACATAA TATTTTTTA

1210 1220 1230 1240 1250
ATTATTCAAA ATAAATATTT TTAAACATCA TATAAAAGAA ATACGACAAA

1260 1270 1280 1290 1300
AAAATTGAGA CGGGAGAAGA CAAGCCAGAC AAAAATGTCC AAGAAACTCT

1310 1320 1330 1340 1350
TTCGTCTAAA TATCTCTCAT CCAAACATAAT ATAATACCCA TTATAATTAA

1360 1370 1380 1390 1400
CCATATTGAC CAACTCAAAC CCCTTAAAT CTATAAATAG ACAAAACCTT

1410 1420 1430 1440 1450
CCCATACCTC TTATCATAAA AAAAATAATA ATCTTTTCA ATAGACAAGT

1460 1470 1480 1490 1500
TTAAAAACCA TACCATATAA CAATATATCA TGGTTATCCA AAGGAATAGT

FIGURE 8B

1510 1520 1530 1540 1550
ATTCTCCTTC TCATTATTAT TTTTGCTTCA TCAATTCAA CTTGTAGAAG

1560 1570 1580 1590 1600
CAATGTTATT GATGACAATT TATTCAAACCA AGTTTATGAT AATATTCTTG

1610 1620 1630 1640 1650
AACAAAGAATT TGCTCATGAT TTTCAAGCTT ATCTTTCTTA TTTGAGCAAA

1660 1670 1680 1690 1700
AATATTGAAA GCAACAATAA TATTGACAAG GTTGATAAAA ATGGGATTAA

1710 1720 1730 1740 1750
AGTGATTAAT GTACTTAGCT TTGGAGCTAA GGGTGATGGA AAAACATATG

1760 1770 1780 1790 1800
ATAATATTGT AAGTATTAA ATATTGGAAT ATATTTGTGG GGATGAAAAT

1810 1820 1830 1840 1850
GATAGAGAAT ATAAGAATTA TTTGGAAGGA TGAAAAGTTA TATTTTATAA

1860 1870 1880 1890 1900
AGTAGAAAAT TATTTTCTCG TTTTTAGTAA TTAAAGGTGA AAAATGAGTT

1910 1920 1930 1940 1950
TTCTCGTAAG CGAGGAAAGT CATTTCAT GGAACGTAT TTTTTTTTA

1960 1970 1980 1990 2000
CTTTTAATAA CGTCATAGTA TTTGCTATAC TCAAGAATAA GACACTATTA

2010 2020 2030 2040 2050
TTGATGTTA GTGCTCGAAA AGAAATTGAT AGTAATTTG CTAATATAAC

2060 2070 2080 2090 2100
TATCAATTTC TTATATGTAT ATTTTCAAC CAAAATAACA AAGCGTAATC

2110 2120 2130 2140 2150
CAATAAGTGG GCCTCTAGAA TAAAGAGTAA GTTCTATTAA TTCTAACCT

2160 2170 2180 2190 2200
TATTTAATT TATGGAAACC TCGACAAAAC GACAATGCTC AACTTATATT

CGAATTTC

FIGURE 8C

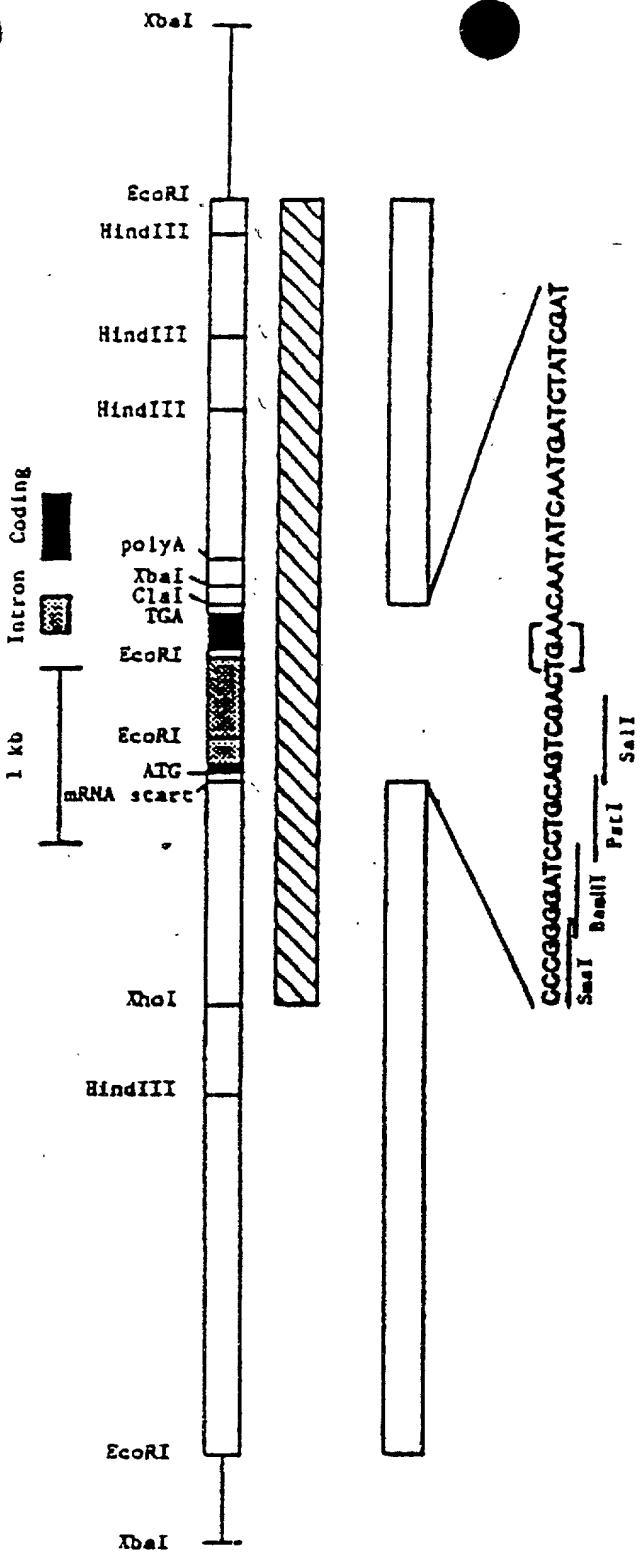


FIGURE 9

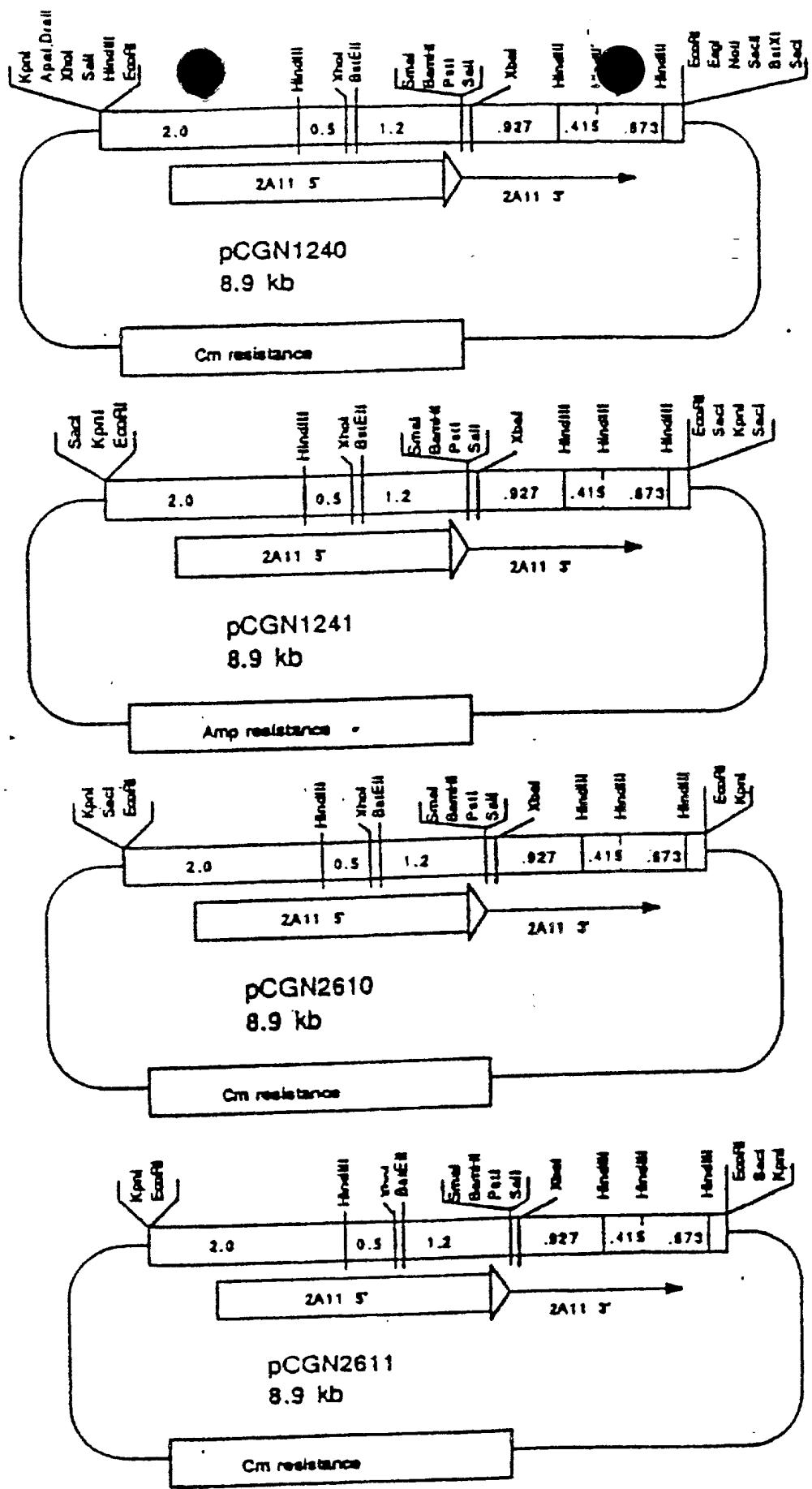


FIGURE 10